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Oct 17 2006 07:23:06

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:25:08 ; Search time 301 Seconds  
 (without alignments)  
 491.703 Million cell updates/sec

Title: US-10-613-744-16

Perfect score: 160

Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt\_7.2;\*  
 1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result No.	Score	Query Match	Length	DB ID	Description
<hr/>					
1	96	60.0	160	1 KCSA_STRCO	P0a333 streptomyce
2	96	60.0	160	1 KCSA_STRLI	P0a334 streptomyce
3	11	6.9	391	2 Q3ICG3_PSEHT	Q3icg3 pseudoalter
4	10	6.2	341	2 Q87YL1_PSESM	Q87yl1 pseudomonas
5	10	6.2	677	1 Y1836_MYCTU	Q50597 mycobacteri
6	10	6.2	677	2 Q7TZG6_MYCBO	Q7tzg6 mycobacteri
7	9	5.6	228	2 Q5BBY5_EMENI	Q5bbby5 aspergillus
8	9	5.6	234	2 Q4EF07_LISMO	Q4ef07 listeria mo
9	9	5.6	234	2 Q4EN54_LISMO	Q4en54 listeria mo
10	9	5.6	234	2 Q71XV5_LISMF	Q71xv5 listeria mo
11	9	5.6	236	2 Q4HYQ6_GIBZE	Q4hyq6 gibberella
12	9	5.6	242	2 Q38WI0_LACSS	Q38wi0 lactobacill
13	9	5.6	247	2 Q8Y5K1_LISMO	Q8y5k1 listeria mo
14	9	5.6	247	2 Q929V8_LISIN	Q929v8 listeria in
15	9	5.6	248	2 Q74JK9_LACJO	Q74jk9 lactobacill
16	9	5.6	258	2 Q88WC7_LACPL	Q88wc7 lactobacill
17	9	5.6	261	2 Q3C8L9_9CLOT	Q3c8l9 alkaliphilu
18	9	5.6	262	2 Q4WQM0_ASPFU	Q4wqm0 aspergillus
19	9	5.6	295	1 KVAP_AERPE	Q9ydf8 aeropyrum p
20	9	5.6	353	2 Q4II59_GIBZE	Q4ii59 gibberella

21	9	5.6	411	2	Q9HP16_HALSA	Q9hp16 halobacteri
22	9	5.6	437	2	Q8XTN1_RALSO	Q8xtn1 ralstonia s
23	9	5.6	455	2	O67715_AQUAE	O67715 aquifex aeo
24	9	5.6	487	2	Q417Y0_KINRA	Q417y0 kineococcus
25	9	5.6	490	2	Q38UF7_LACSS	Q38uf7 lactobacill
26	9	5.6	1017	2	Q33UI1_9GAMM	Q33ui1 shewanella
27	8	5.0	70	2	O04227_PLAMJ	O04227 plantago ma
28	8	5.0	72	2	O04236_VICFA	O04236 vicia faba
29	8	5.0	72	2	O04241_MAIZE	O04241 zea mays (m
30	8	5.0	79	1	TATA_HELPJ	Q9zmb8 helicobacte
31	8	5.0	79	1	TATA_HELPY	O25088 helicobacte
32	8	5.0	88	2	Q6KFT9_ATEGE	Q6kft9 ateles geof
33	8	5.0	97	2	O57411_CHICK	O57411 gallus gall
34	8	5.0	104	2	Q7U629_SYNPX	Q7u629 synechococc
35	8	5.0	120	2	Q5Z188_NOFCFA	Q5z188 nocardia fa
36	8	5.0	131	2	Q4IPG7_GIBZE	Q4ipg7 gibberella
37	8	5.0	134	2	Q2J959_9ACTO	Q2j959 frankia sp.
38	8	5.0	150	2	Q3H4X4_9ACTO	Q3h4x4 nocardioide
39	8	5.0	154	2	Q3SNH6_NITWN	Q3snh6 nitrobacter
40	8	5.0	191	2	Q9LKP1_MESCR	Q9lkp1 mesembryant
41	8	5.0	193	2	Q3FX17_9BURK	Q3fx17 rhodoferax
42	8	5.0	223	2	Q8PW61_METMA	Q8pw61 methanosarc
43	8	5.0	233	2	Q3H543_9ACTO	Q3h543 nocardioide
44	8	5.0	244	2	Q4NH76_9MICC	Q4nh76 arthrobacte
45	8	5.0	247	2	Q3IPV9_NATPD	Q3ipv9 natronomona

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## OM protein - protein search, using sw model

Run on: October 6, 2006, 18:10:18 ; Search time 200 Seconds  
(without alignments)  
365.773 Million cell updates/sec

Title: US-10-613-744-16

Perfect score: 816

Sequence: 1 MPPMLSGLLARLVKLLLGRH . . . . . TRALHERFDRLERMLDDNRR 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs;\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
1	816	100.0	160	2	AAY32024	Aay32024 Streptomy
2	816	100.0	160	8	ADI38338	Adi38338 S. livida
3	816	100.0	160	10	AEE68564	Aee68564 Streptomy
4	800	98.0	160	2	AAY32009	Aay32009 Streptomy
5	800	98.0	160	8	ADI38323	Adi38323 Streptomy
6	800	98.0	160	10	AEE68549	Aee68549 Streptomy
7	791	96.9	183	5	AAG80259	Aag80259 Chimeric
8	784	96.1	183	5	AAG80262	Aag80262 Chimeric
9	765	93.8	183	5	AAG80261	Aag80261 Chimeric
10	764	93.6	183	5	AAG80258	Aag80258 Chimeric
11	762	93.4	183	5	AAG80260	Aag80260 Chimeric
12	761	93.3	183	5	AAG80263	Aag80263 Chimeric

13	761	93.3	183	5	AAG80264	Aag80264 Chimeric
14	760	93.1	183	5	AAG80257	Aag80257 Chimeric
15	754	92.4	183	5	AAG80265	Aag80265 Chimeric
16	738	90.4	183	5	AAG80256	Aag80256 Chimeric
17	723	88.6	183	5	AAG80255	Aag80255 Chimeric
18	431	52.8	90	3	AAY83193	Aay83193 Transmemb
19	431	52.8	90	6	ABU09828	Abu09828 Membrane
20	431	52.8	90	6	ABG71875	Abg71875 S. livida
21	296	36.3	58	8	ADI38363	Adi38363 Streptomy
22	296	36.3	58	10	AEE68573	Aee68573 S. livida
23	283	34.7	59	3	AAY83192	Aay83192 Transmemb
24	283	34.7	59	6	ABU09827	Abu09827 Membrane
25	283	34.7	59	6	ABG71874	Abg71874 S. livida
26	222	27.2	280	6	ABU49669	Abu49669 Protein e
27	192	23.5	40	2	AAY32028	Aay32028 Streptomy
28	192	23.5	40	8	ADI38345	Adi38345 Streptomy
29	192	23.5	40	10	AEE68571	Aee68571 Streptomy
30	191	23.4	257	8	ADK48074	Adk48074 Streptoco
31	189	23.2	287	8	ADR96037	Adr96037 Novel S.
32	189	23.2	287	9	AEA59907	Aea59907 Streptoco
33	181	22.2	249	4	AAU87098	Aau87098 Novel cen
34	181	22.2	249	8	ADI54413	Adi54413 Novel hum
35	181	22.2	250	4	AAU18283	Aau18283 Human end
36	181	22.2	523	6	ABR42417	Abr42417 Human pot
37	181	22.2	523	7	ADJ70209	Adj70209 Human hea
38	181	22.2	523	8	ADR40129	Adr40129 Human vol
39	181	22.2	523	8	ABO84782	Abo84782 Human can
40	181	22.2	523	9	ADZ13401	Adz13401 Human can
41	181	22.2	523	9	ADZ13399	Adz13399 Human can
42	181	22.2	523	9	ADZ13403	Adz13403 Human can
43	181	22.2	528	8	ABO84781	Abo84781 Murine ca
44	181	22.2	528	9	ADZ13396	Adz13396 Murine ca
45	180	22.1	393	2	AAW14282	Aaw14282 Human K+

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:34:33 ; Search time 188 Seconds  
(without alignments)  
394.225 Million cell updates/sec

Title: US-10-613-744-16  
Perfect score: 160  
Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2094455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	160	100.0	160	5	US-10-613-744-16	Sequence 16, Appl
2	96	60.0	160	5	US-10-613-744-1	Sequence 1, Appl
3	54	33.8	58	5	US-10-613-744-25	Sequence 25, Appl
4	50	31.2	90	4	US-10-203-578-1	Sequence 1, Appl
5	48	30.0	59	4	US-10-207-330-16	Sequence 16, Appl
6	48	30.0	90	4	US-10-207-330-17	Sequence 17, Appl
7	31	19.4	31	4	US-10-207-330-15	Sequence 15, Appl
8	25	15.6	40	5	US-10-613-744-23	Sequence 23, Appl
9	22	13.8	36	5	US-10-613-744-41	Sequence 41, Appl
10	10	6.2	341	4	US-10-282-122A-69276	Sequence 69276, A
11	10	6.2	677	4	US-10-080-170-488	Sequence 488, App
12	10	6.2	677	4	US-10-080-170-488	Sequence 488, App
13	10	6.2	677	4	US-10-468-356-488	Sequence 488, App
14	9	5.6	247	4	US-10-282-122A-60781	Sequence 60781, A
15	9	5.6	247	6	US-11-045-004-1955	Sequence 1955, Ap
16	9	5.6	250	5	US-10-724-264A-123	Sequence 123, App

17	9	5.6	295	4	US-10-377-139-1	Sequence 1, Appli
18	9	5.6	383	4	US-10-424-599-158630	Sequence 158630,
19	8	5.0	25	3	US-09-086-436-46	Sequence 46, Appl
20	8	5.0	25	4	US-10-753-991-46	Sequence 46, Appl
21	8	5.0	25	5	US-10-384-107-39	Sequence 39, Appl
22	8	5.0	58	5	US-10-613-744-34	Sequence 34, Appl
23	8	5.0	63	3	US-09-894-882-347	Sequence 347, App
24	8	5.0	63	5	US-10-894-314A-347	Sequence 347, App
25	8	5.0	79	4	US-10-023-171-15	Sequence 15, Appl
26	8	5.0	79	4	US-10-424-599-242319	Sequence 242319,
27	8	5.0	176	4	US-10-425-115-261936	Sequence 261936,
28	8	5.0	326	4	US-10-425-114-70837	Sequence 70837, A
29	8	5.0	347	4	US-10-389-566-2029	Sequence 2029, Ap
30	8	5.0	348	4	US-10-389-566-783	Sequence 783, App
31	8	5.0	348	4	US-10-389-566-2438	Sequence 2438, Ap
32	8	5.0	349	4	US-10-389-566-1121	Sequence 1121, Ap
33	8	5.0	349	4	US-10-389-566-2098	Sequence 2098, Ap
34	8	5.0	349	4	US-10-389-566-2148	Sequence 2148, Ap
35	8	5.0	349	4	US-10-437-963-190619	Sequence 190619,
36	8	5.0	352	4	US-10-389-566-2165	Sequence 2165, Ap
37	8	5.0	360	4	US-10-425-115-261948	Sequence 261948,
38	8	5.0	363	4	US-10-389-566-1256	Sequence 1256, Ap
39	8	5.0	363	4	US-10-389-566-1609	Sequence 1609, Ap
40	8	5.0	363	4	US-10-389-566-1649	Sequence 1649, Ap
41	8	5.0	414	5	US-10-450-763-31371	Sequence 31371, A
42	8	5.0	421	4	US-10-369-493-6429	Sequence 6429, Ap
43	8	5.0	460	4	US-10-369-493-5528	Sequence 5528, Ap
44	8	5.0	487	4	US-10-389-647-614	Sequence 614, App
45	8	5.0	490	4	US-10-369-493-5896	Sequence 5896, Ap

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:33:48 ; Search time 53 Seconds  
 (without alignments)  
 264.243 Million cell updates/sec

Title: US-10-613-744-16  
 Perfect score: 160  
 Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 645225

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query				Description
No.	Score	Match	Length	DB ID	
<hr/>					
1	160	100.0	160	2 US-09-275-252A-16	Sequence 16, Appl
2	96	60.0	160	2 US-09-275-252A-1	Sequence 1, Appl
3	54	33.8	58	2 US-09-275-252A-25	Sequence 25, Appl
4	48	30.0	59	2 US-09-384-302A-16	Sequence 16, Appl
5	48	30.0	90	2 US-09-384-302A-17	Sequence 17, Appl
6	31	19.4	31	2 US-09-384-302A-15	Sequence 15, Appl
7	25	15.6	40	2 US-09-275-252A-23	Sequence 23, Appl
8	22	13.8	36	2 US-09-275-252A-41	Sequence 41, Appl
9	8	5.0	25	2 US-08-997-685A-39	Sequence 39, Appl
10	8	5.0	25	2 US-09-086-436-46	Sequence 46, Appl
11	8	5.0	27	2 US-08-749-816-15	Sequence 15, Appl
12	8	5.0	58	2 US-09-275-252A-34	Sequence 34, Appl
13	8	5.0	63	2 US-09-894-882-347	Sequence 347, App
14	8	5.0	79	2 US-09-053-197A-15	Sequence 15, Appl
15	8	5.0	79	2 US-09-085-761A-15	Sequence 15, Appl

16	8	5.0	127	2	US-09-902-540-14613	Sequence 14613, A
17	8	5.0	440	2	US-09-252-991A-29525	Sequence 29525, A
18	8	5.0	857	2	US-09-275-252A-11	Sequence 11, Appl
19	8	5.0	1427	2	US-09-252-991A-20577	Sequence 20577, A
20	7	4.4	15	2	US-09-336-643A-68	Sequence 68, Appl
21	7	4.4	15	2	US-09-336-643A-71	Sequence 71, Appl
22	7	4.4	17	1	US-08-103-445-6	Sequence 6, Appl
23	7	4.4	17	1	US-08-103-445-7	Sequence 7, Appl
24	7	4.4	17	1	US-08-461-690B-6	Sequence 6, Appl
25	7	4.4	17	1	US-08-461-690B-7	Sequence 7, Appl
26	7	4.4	25	1	US-07-921-178A-3	Sequence 3, Appl
27	7	4.4	25	1	US-07-921-178A-4	Sequence 4, Appl
28	7	4.4	25	1	US-07-921-178A-7	Sequence 7, Appl
29	7	4.4	25	1	US-07-921-178A-8	Sequence 8, Appl
30	7	4.4	25	1	US-07-921-178A-9	Sequence 9, Appl
31	7	4.4	25	2	US-08-997-685A-36	Sequence 36, Appl
32	7	4.4	25	2	US-08-997-685A-37	Sequence 37, Appl
33	7	4.4	25	2	US-09-922-364A-45	Sequence 45, Appl
34	7	4.4	25	2	US-09-086-436-43	Sequence 43, Appl
35	7	4.4	25	2	US-09-086-436-44	Sequence 44, Appl
36	7	4.4	25	2	US-09-254-590-45	Sequence 45, Appl
37	7	4.4	25	2	US-10-115-415-45	Sequence 45, Appl
38	7	4.4	25	2	US-10-116-260-45	Sequence 45, Appl
39	7	4.4	25	2	US-10-115-671-45	Sequence 45, Appl
40	7	4.4	25	2	US-10-115-695-45	Sequence 45, Appl
41	7	4.4	25	2	US-10-116-561-45	Sequence 45, Appl
42	7	4.4	25	3	US-10-115-688-45	Sequence 45, Appl
43	7	4.4	27	2	US-08-749-816-10	Sequence 10, Appl
44	7	4.4	27	2	US-08-749-816-11	Sequence 11, Appl
45	7	4.4	27	2	US-08-749-816-13	Sequence 13, Appl

# **SCORE Search Results Details for Application 10613744 and Search Result us-10-613-744- 16.olig.rapbn.**

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This page gives you Search Results detail for the Application 10613744 and Search Result us-10-613-744-16.olig.rapbn.

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:35:28 ; Search time 38 Seconds  
(without alignments)  
332.355 Million cell updates/sec

Title: US-10-613-744-16

Perfect score: 160

Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 291792 seqs, 78934247 residues

Word size : 1

Total number of hits satisfying chosen parameters: 291649

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA\_New:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%	Query
--------	---	-------

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:35:28 ; Search time 38 Seconds  
 (without alignments)  
 332.355 Million cell updates/sec

Title: US-10-613-744-16

Perfect score: 160

Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 291792 seqs, 78934247 residues

Word size : 1

Total number of hits satisfying chosen parameters: 291649

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA\_New:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB ID	
1	8	5.0	204	6 US-10-953-349-8321	Sequence 8321, Ap
2	8	5.0	223	6 US-10-953-349-8320	Sequence 8320, Ap
3	8	5.0	253	6 US-10-953-349-8319	Sequence 8319, Ap
4	8	5.0	323	7 US-11-330-403-11637	Sequence 11637, A
5	8	5.0	347	6 US-10-449-902-47323	Sequence 47323, A
6	8	5.0	349	6 US-10-449-902-40702	Sequence 40702, A
7	8	5.0	943	6 US-10-374-780A-1838	Sequence 1838, Ap
8	7	4.4	24	7 US-11-178-538-11	Sequence 11, Appl
9	7	4.4	24	7 US-11-178-538-13	Sequence 13, Appl
10	7	4.4	24	7 US-11-178-538-14	Sequence 14, Appl
11	7	4.4	40	7 US-11-251-465-39	Sequence 39, Appl
12	7	4.4	84	7 US-11-384-643-22	Sequence 22, Appl
13	7	4.4	85	7 US-11-384-643-18	Sequence 18, Appl
14	7	4.4	85	7 US-11-384-643-20	Sequence 20, Appl

15	7	4.4	156	6	US-10-520-780-12	Sequence 12, Appl
16	7	4.4	157	6	US-10-520-780-8	Sequence 8, Appli
17	7	4.4	159	6	US-10-520-780-5	Sequence 5, Appli
18	7	4.4	160	6	US-10-520-780-6	Sequence 6, Appli
19	7	4.4	161	6	US-10-520-780-7	Sequence 7, Appli
20	7	4.4	164	6	US-10-520-780-9	Sequence 9, Appli
21	7	4.4	171	6	US-10-520-780-10	Sequence 10, Appl
22	7	4.4	182	6	US-10-953-349-29589	Sequence 29589, A
23	7	4.4	182	7	US-11-056-355B-56769	Sequence 56769, A
24	7	4.4	182	7	US-11-056-355B-69221	Sequence 69221, A
25	7	4.4	207	6	US-10-449-902-40660	Sequence 40660, A
26	7	4.4	248	6	US-10-953-349-1842	Sequence 1842, Ap
27	7	4.4	254	7	US-11-056-355B-9740	Sequence 9740, Ap
28	7	4.4	272	7	US-11-056-355B-52834	Sequence 52834, A
29	7	4.4	275	6	US-10-471-571A-2596	Sequence 2596, Ap
30	7	4.4	280	6	US-10-953-349-5590	Sequence 5590, Ap
31	7	4.4	293	6	US-10-471-571A-512	Sequence 512, App
32	7	4.4	304	7	US-11-293-697-4875	Sequence 4875, Ap
33	7	4.4	308	7	US-11-056-355B-52833	Sequence 52833, A
34	7	4.4	316	6	US-10-953-349-1841	Sequence 1841, Ap
35	7	4.4	321	6	US-10-449-902-49359	Sequence 49359, A
36	7	4.4	330	6	US-10-449-902-32175	Sequence 32175, A
37	7	4.4	330	6	US-10-449-902-37113	Sequence 37113, A
38	7	4.4	346	6	US-10-449-902-35539	Sequence 35539, A
39	7	4.4	351	7	US-11-293-697-3961	Sequence 3961, Ap
40	7	4.4	351	7	US-11-317-847A-58	Sequence 58, Appl
41	7	4.4	400	7	US-11-056-355B-52832	Sequence 52832, A
42	7	4.4	407	7	US-11-056-355B-16857	Sequence 16857, A
43	7	4.4	408	6	US-10-953-349-1840	Sequence 1840, Ap
44	7	4.4	425	6	US-10-953-349-33681	Sequence 33681, A
45	7	4.4	425	7	US-11-056-355B-5999	Sequence 5999, Ap

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:28:43 ; Search time 41 Seconds  
 (without alignments)  
 375.480 Million cell updates/sec

Title: US-10-613-744-16  
 Perfect score: 160  
 Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_80:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			DB	ID	Description
		%	Match	Length			
1	96	60.0	160	2	S60172		potassium channel
2	10	6.2	677	2	E70722		hypothetical prote
3	9	5.6	247	2	AC1332		potassium channel
4	9	5.6	247	2	AC1703		potassium channel
5	9	5.6	295	2	C72692		probable potassium
6	9	5.6	411	2	B84336		potassium channel
7	9	5.6	455	2	A70461		potassium channel
8	8	5.0	72	2	T12130		potassium channel
9	8	5.0	72	2	T03391		potassium channel
10	8	5.0	79	1	H64559		conserved hypothet
11	8	5.0	79	2	A71948		hypothetical prote
12	8	5.0	263	2	S76994		hypothetical prote
13	8	5.0	263	2	AI2073		hypothetical prote
14	8	5.0	281	2	E75267		hypothetical prote
15	8	5.0	349	2	T07396		probable outward r
16	8	5.0	421	2	T29789		hypothetical prote
17	8	5.0	460	2	T27759		hypothetical prote
18	8	5.0	487	2	E83120		probable outer mem

19	8	5.0	490	2	T26983	hypothetical prote
20	8	5.0	662	2	T04461	potassium channel
21	8	5.0	787	2	S68699	potassium channel
22	8	5.0	807	2	T12177	potassium channel
23	8	5.0	838	2	S23606	potassium channel
24	8	5.0	845	2	T07052	probable potassium
25	8	5.0	857	2	S62694	potassium channel
26	8	5.0	883	2	T07651	potassium channel
27	8	5.0	887	2	T03939	potassium channel
28	7	4.4	37	2	T07292	hypothetical prote
29	7	4.4	44	2	S29975	hypA protein - Alc
30	7	4.4	57	2	S09042	potassium channel
31	7	4.4	57	2	S09045	potassium channel
32	7	4.4	57	2	S09044	potassium channel
33	7	4.4	57	2	S09048	potassium channel
34	7	4.4	57	2	S09047	potassium channel
35	7	4.4	57	2	S09043	potassium channel
36	7	4.4	74	2	AH3307	transcription regu
37	7	4.4	81	2	B91251	hypothetical prote
38	7	4.4	84	2	S29892	hypothetical prote
39	7	4.4	87	2	F84161	hypothetical prote
40	7	4.4	88	2	A70895	hypothetical prote
41	7	4.4	97	2	T28909	hypothetical prote
42	7	4.4	101	2	B87208	probable secreted
43	7	4.4	102	2	A83553	hypothetical prote
44	7	4.4	104	2	E69405	hypothetical prote
45	7	4.4	116	2	H75601	hypothetical prote

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:24:28 ; Search time 201 Seconds  
(without alignments)  
363.953 Million cell updates/sec

Title: US-10-613-744-16  
Perfect score: 160  
Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2588247

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
1	160	100.0	160	2	AAY32024		Aay32024 Streptomy
2	160	100.0	160	8	ADI38338		Adi38338 S. livida
3	160	100.0	160	10	AEE68564		Aee68564 Streptomy
4	98	61.3	183	5	AAG80258		Aag80258 Chimeric
5	98	61.3	183	5	AAG80263		Aag80263 Chimeric
6	98	61.3	183	5	AAG80264		Aag80264 Chimeric
7	98	61.3	183	5	AAG80265		Aag80265 Chimeric
8	98	61.3	183	5	AAG80259		Aag80259 Chimeric
9	96	60.0	160	2	AAY32009		Aay32009 Streptomy
10	96	60.0	160	8	ADI38323		Adi38323 Streptomy
11	96	60.0	160	10	AEE68549		Aee68549 Streptomy
12	94	58.8	183	5	AAG80257		Aag80257 Chimeric

13	79	49.4	183	5	AAG80260	Aag80260 Chimeric
14	78	48.8	183	5	AAG80262	Aag80262 Chimeric
15	73	45.6	183	5	AAG80261	Aag80261 Chimeric
16	73	45.6	183	5	AAG80255	Aag80255 Chimeric
17	73	45.6	183	5	AAG80256	Aag80256 Chimeric
18	54	33.8	58	8	ADI38363	Adi38363 Streptomy
19	54	33.8	58	10	AEE68573	Aee68573 S. livida
20	48	30.0	59	3	AAY83192	Aay83192 Transmemb
21	48	30.0	59	6	ABU09827	Abu09827 Membrane
22	48	30.0	59	6	ABG71874	Abg71874 S. livida
23	48	30.0	90	3	AAY83193	Aay83193 Transmemb
24	48	30.0	90	6	ABU09828	Abu09828 Membrane
25	48	30.0	90	6	ABG71875	Abg71875 S. livida
26	31	19.4	31	3	AAY83191	Aay83191 Transmemb
27	31	19.4	31	6	ABU09826	Abu09826 Membrane
28	31	19.4	31	6	ABG71873	Abg71873 S. livida
29	25	15.6	40	2	AAY32028	Aay32028 Streptomy
30	25	15.6	40	8	ADI38345	Adi38345 Streptomy
31	25	15.6	40	10	AEE68571	Aee68571 Streptomy
32	22	13.8	36	8	ADI38361	Adi38361 Streptomy
33	22	13.8	36	10	AEE68589	Aee68589 Streptomy
34	21	13.1	23	7	ADC89699	Adc89699 KcsA pept
35	19	11.9	21	3	AAB11387	Aab11387 Potassium
36	10	6.2	341	6	ABU41352	Abu41352 Protein e
37	10	6.2	677	5	ABU05837	Abu05837 M. tuberc
38	9	5.6	247	5	ABB49250	Abb49250 Listeria
39	9	5.6	247	6	ABU32857	Abu32857 Protein e
40	9	5.6	250	8	ADQ82628	Adq82628 Wild type
41	9	5.6	295	8	ADS16289	Ads16289 Aeropyrum
42	8	5.0	58	8	ADI38354	Adi38354 Arabidops
43	8	5.0	58	10	AEE68582	Aee68582 Mouse-ear
44	8	5.0	63	5	ABB88780	Abb88780 Conus str
45	8	5.0	79	2	AAW20453	Aaw20453 H. pylori

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:19:38 ; Search time 52 Seconds  
 (without alignments)  
 269.325 Million cell updates/sec

Title: US-10-613-744-16  
 Perfect score: 816  
 Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query				Description
No.	Score	Match	Length	DB	ID
<hr/>					
1	816	100.0	160	2	US-09-275-252A-16
2	800	98.0	160	2	US-09-275-252A-1
3	431	52.8	90	2	US-09-384-302A-17
4	296	36.3	58	2	US-09-275-252A-25
5	283	34.7	59	2	US-09-384-302A-16
6	192	23.5	40	2	US-09-275-252A-23
7	191	23.4	257	2	US-09-583-110-4589
8	189	23.2	287	2	US-09-107-433-4672
9	185	22.7	528	1	US-08-527-152-2
10	181	22.2	523	2	US-09-949-016-6195
11	181	22.2	552	2	US-09-949-016-8164
12	180	22.1	722	2	US-09-105-058C-23
13	180	22.1	844	2	US-09-813-148-4
14	180	22.1	844	2	US-09-590-304-4
15	180	22.1	844	2	US-09-492-361-34

16	180	22.1	844	2	US-09-866-020A-29	Sequence 29, Appl
17	180	22.1	871	2	US-09-105-058C-20	Sequence 20, Appl
18	180	22.1	872	2	US-09-177-650-2	Sequence 2, Appl
19	180	22.1	930	2	US-09-177-650-96	Sequence 96, Appl
20	179	21.9	36	2	US-09-275-252A-41	Sequence 41, Appl
21	177.5	21.8	616	2	US-09-275-252A-4	Sequence 4, Appl
22	177	21.7	245	2	US-09-105-058C-8	Sequence 8, Appl
23	177	21.7	300	2	US-09-105-058C-4	Sequence 4, Appl
24	177	21.7	300	2	US-09-105-058C-6	Sequence 6, Appl
25	177	21.7	757	2	US-09-177-650-89	Sequence 89, Appl
26	170.5	20.9	529	2	US-09-949-016-6196	Sequence 6196, Ap
27	170.5	20.9	538	2	US-09-949-016-8017	Sequence 8017, Ap
28	169	20.7	495	2	US-09-275-252A-5	Sequence 5, Appl
29	169	20.7	854	2	US-09-590-304-7	Sequence 7, Appl
30	169	20.7	897	2	US-09-590-304-2	Sequence 2, Appl
31	169	20.7	897	2	US-09-866-020A-2	Sequence 2, Appl
32	169	20.7	923	2	US-09-825-147-2	Sequence 2, Appl
33	169	20.7	932	2	US-09-813-148-2	Sequence 2, Appl
34	168	20.6	676	2	US-09-949-016-7694	Sequence 7694, Ap
35	168	20.6	695	2	US-09-590-304-6	Sequence 6, Appl
36	168	20.6	695	2	US-09-492-361-2	Sequence 2, Appl
37	168	20.6	695	2	US-09-866-020A-31	Sequence 31, Appl
38	168	20.6	696	2	US-09-813-148-6	Sequence 6, Appl
39	164	20.1	261	2	US-09-134-000C-5295	Sequence 5295, Ap
40	163	20.0	806	2	US-09-833-466-13	Sequence 13, Appl
41	162.5	19.9	310	2	US-09-105-058C-18	Sequence 18, Appl
42	162.5	19.9	376	2	US-09-135-020-113	Sequence 113, App
43	162.5	19.9	376	2	US-09-135-010A-113	Sequence 113, App
44	162.5	19.9	376	2	US-09-444-871-113	Sequence 113, App
45	162.5	19.9	376	2	US-09-597-735-113	Sequence 113, App

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: October 6, 2006, 18:20:18 ; Search time 182 Seconds  
 (without alignments)  
 407.222 Million cell updates/sec

Title: US-10-613-744-16

Perfect score: 816

Sequence: 1 MPPMLSGLLARLVKLLLGRH.....TRALHERFDRLERMLDDNRR 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB ID	
1	816	100.0	160	5 US-10-613-744-16	Sequence 16, Appl
2	800	98.0	160	5 US-10-613-744-1	Sequence 1, Appl
3	444	54.4	90	4 US-10-203-578-1	Sequence 1, Appl
4	431	52.8	90	4 US-10-207-330-17	Sequence 17, Appl
5	296	36.3	58	5 US-10-613-744-25	Sequence 25, Appl
6	283	34.7	59	4 US-10-207-330-16	Sequence 16, Appl
7	232	28.4	275	4 US-10-156-761-13328	Sequence 13328, A
8	222	27.2	280	4 US-10-282-122A-77593	Sequence 77593, A
9	192	23.5	40	5 US-10-613-744-23	Sequence 23, Appl
10	189	23.2	287	5 US-10-617-320-4672	Sequence 4672, Ap
11	181	22.2	249	3 US-09-764-875-616	Sequence 616, App
12	181	22.2	521	4 US-10-322-281-96	Sequence 96, Appl
13	181	22.2	523	3 US-09-804-014A-32	Sequence 32, Appl
14	181	22.2	523	4 US-10-408-765A-2015	Sequence 2015, Ap
15	181	22.2	523	5 US-10-772-636-10	Sequence 10, Appl
16	181	22.2	523	6 US-11-288-493-10	Sequence 10, Appl

17	181	22.2	524	4	US-10-322-281-93	Sequence 93, Appl
18	181	22.2	525	3	US-09-804-014A-33	Sequence 33, Appl
19	180	22.1	393	4	US-10-116-712-665	Sequence 665, App
20	180	22.1	615	4	US-10-744-796-6	Sequence 6, Appli
21	180	22.1	625	4	US-10-744-796-4	Sequence 4, Appli
22	180	22.1	643	4	US-10-744-796-2	Sequence 2, Appli
23	180	22.1	722	4	US-10-128-870-23	Sequence 23, Appl
24	180	22.1	722	4	US-10-131-685-23	Sequence 23, Appl
25	180	22.1	842	4	US-10-820-307-3	Sequence 3, Appli
26	180	22.1	844	3	US-09-866-020-30	Sequence 30, Appl
27	180	22.1	844	3	US-09-813-148-4	Sequence 4, Appli
28	180	22.1	844	3	US-09-810-796-14	Sequence 14, Appl
29	180	22.1	844	4	US-10-295-027-282	Sequence 282, App
30	180	22.1	844	4	US-10-661-629-4	Sequence 4, Appli
31	180	22.1	844	5	US-10-643-795A-152	Sequence 152, App
32	180	22.1	844	5	US-10-850-928-34	Sequence 34, Appl
33	180	22.1	844	5	US-10-948-493-29	Sequence 29, Appl
34	180	22.1	844	5	US-10-948-518-152	Sequence 152, App
35	180	22.1	844	5	US-10-482-834A-161	Sequence 161, App
36	180	22.1	844	5	US-10-287-436A-601	Sequence 601, App
37	180	22.1	852	4	US-10-820-307-9	Sequence 9, Appli
38	180	22.1	871	4	US-10-128-870-20	Sequence 20, Appl
39	180	22.1	871	4	US-10-131-685-20	Sequence 20, Appl
40	180	22.1	872	4	US-10-345-680-17	Sequence 17, Appl
41	180	22.1	872	4	US-10-096-578-2	Sequence 2, Appli
42	180	22.1	872	4	US-10-820-307-2	Sequence 2, Appli
43	180	22.1	872	4	US-10-744-796-7	Sequence 7, Appli
44	180	22.1	912	5	US-10-450-763-41003	Sequence 41003, A
45	180	22.1	914	5	US-10-450-763-41002	Sequence 41002, A

GenCore version 5.1.9

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### OM protein - protein search, using sw model

Run on: October 6, 2006, 18:21:18 ; Search time 37 Seconds  
(without alignments)  
341.337 Million cell updates/sec

Title: US-10-613-744-16

Perfect score: 816

Sequence: 1 MPPMLSGLLARLVKLLLGRH. . . . . . . TRALHERFDRLERMLDDNRR 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 291792 seqs, 78934247 residues

Total number of hits satisfying chosen parameters: 291792

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

```
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query					Description
		Match	Length	DB	ID		
<hr/>							
1	181	22.2	521	6	US-10-539-228-96	Sequence 96, Appl	
2	181	22.2	521	6	US-10-669-920-919	Sequence 919, Appl	
3	181	22.2	521	6	US-10-669-920-921	Sequence 921, Appl	
4	181	22.2	521	6	US-10-669-920-923	Sequence 923, Appl	
5	181	22.2	523	7	US-11-313-450-21	Sequence 21, Appl	
6	181	22.2	524	6	US-10-539-228-93	Sequence 93, Appl	
7	181	22.2	524	6	US-10-669-920-916	Sequence 916, Appl	
8	180	22.1	393	7	US-11-363-917-5	Sequence 5, Appl	
9	180	22.1	615	6	US-10-519-335-6	Sequence 6, Appl	
10	180	22.1	625	6	US-10-519-335-4	Sequence 4, Appl	
11	180	22.1	643	6	US-10-519-335-2	Sequence 2, Appl	
12	180	22.1	854	7	US-11-363-917-3	Sequence 3, Appl	
13	180	22.1	872	6	US-10-519-335-7	Sequence 7, Appl	
14	180	22.1	872	7	US-11-302-678-17	Sequence 17, Appl	

15	173.5	21.3	157	6	US-10-520-780-8	Sequence 8, Appli
16	172.5	21.1	171	6	US-10-520-780-10	Sequence 10, Appl
17	170.5	20.9	529	7	US-11-312-958-26	Sequence 26, Appl
18	169.5	20.8	653	7	US-11-313-450-22	Sequence 22, Appl
19	169	20.7	495	7	US-11-313-450-19	Sequence 19, Appl
20	167.5	20.5	161	6	US-10-520-780-7	Sequence 7, Appli
21	166	20.3	613	7	US-11-313-450-23	Sequence 23, Appl
22	166	20.3	639	7	US-11-317-847A-98	Sequence 98, Appl
23	164	20.1	159	6	US-10-520-780-5	Sequence 5, Appli
24	163	20.0	911	7	US-11-313-450-25	Sequence 25, Appl
25	162.5	19.9	581	7	US-11-363-917-6	Sequence 6, Appli
26	162.5	19.9	825	7	US-11-363-917-8	Sequence 8, Appli
27	161.5	19.8	164	6	US-10-520-780-9	Sequence 9, Appli
28	161.5	19.8	872	7	US-11-363-917-7	Sequence 7, Appli
29	160	19.6	858	7	US-11-313-450-24	Sequence 24, Appl
30	160	19.6	972	7	US-11-317-847A-100	Sequence 100, App
31	158.5	19.4	465	7	US-11-317-847A-82	Sequence 82, Appl
32	158.5	19.4	465	7	US-11-317-847A-84	Sequence 84, Appl
33	158.5	19.4	465	7	US-11-317-847A-86	Sequence 86, Appl
34	158.5	19.4	465	7	US-11-317-847A-88	Sequence 88, Appl
35	158.5	19.4	581	7	US-11-317-847A-90	Sequence 90, Appl
36	158.5	19.4	586	7	US-11-317-847A-92	Sequence 92, Appl
37	158.5	19.4	589	7	US-11-317-847A-94	Sequence 94, Appl
38	158.5	19.4	603	7	US-11-317-847A-96	Sequence 96, Appl
39	155	19.0	494	7	US-11-251-465-17	Sequence 17, Appl
40	154.5	18.9	499	6	US-10-539-228-763	Sequence 763, App
41	154.5	18.9	499	6	US-10-669-920-926	Sequence 926, App
42	154.5	18.9	612	7	US-11-317-847A-104	Sequence 104, App
43	154.5	18.9	616	7	US-11-317-847A-106	Sequence 106, App
44	153.5	18.8	160	6	US-10-520-780-6	Sequence 6, Appli
45	153.5	18.8	499	6	US-10-539-228-766	Sequence 766, App

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## OM protein - protein search, using sw model

Run on: October 6, 2006, 18:14:33 ; Search time 40 Seconds  
(without alignments)  
384.867 Million cell updates/sec

Title: US-10-613-744-16

Perfect score: 816

Sequence: 1 MPPMLSGLLARLVKLLLGRH. . . . . TRALHERFDRLERMLDDNRR 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:\*

1: pirl:\*

2: pir2:\*

3: pir3:\*

4 : pir4 : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

四

Result No.	Score	Match Length	DB	ID	Description
1	800	98.0	160	2 S60172	potassium channel
2	222	27.2	280	2 C82490	probable potassium
3	185	22.7	528	2 I84205	potassium channel
4	181	22.2	523	2 A38101	potassium channel
5	181	22.2	525	2 A43531	potassium channel
6	180	22.1	393	2 JC5275	voltage-gated pota
7	176.5	21.6	247	2 AC1703	potassium channel
8	176.5	21.6	256	2 E69166	conserved hypothet
9	176.5	21.6	295	2 C72692	probable potassium
10	176	21.6	602	2 A49507	potassium channel
11	175.5	21.5	140	2 B86739	potassium channel
12	174	21.3	247	2 AC1332	potassium channel
13	173.5	21.3	643	2 S00480	potassium channel
14	173.5	21.3	656	2 JH0193	potassium channel
15	170.5	20.9	529	2 S12787	potassium channel
16	170	20.8	489	2 I51532	potassium channel
17	170	20.8	598	2 S66669	potassium channel
18	170	20.8	602	2 JH0166	potassium voltage-

19	170	20.8	645	2	T27186	hypothetical prote
20	169.5	20.8	530	2	JH0167	potassium channel
21	169.5	20.8	653	2	A39922	potassium channel
22	169.5	20.8	654	2	S11049	potassium channel
23	169.5	20.8	660	2	S24125	potassium channel
24	169	20.7	495	2	I57680	potassium channel
25	168	20.6	495	2	A40090	potassium channel
26	168	20.6	495	2	B39113	potassium channel
27	166	20.3	613	2	A56031	potassium channel
28	163	20.0	514	2	C49507	potassium channel
29	163	20.0	802	2	JH0595	potassium channel
30	160	19.6	597	2	S51212	BAK5 protein - bov
31	160	19.6	853	1	CHRTD1	potassium channel
32	160	19.6	857	2	I56529	potassium channel
33	160	19.6	858	2	S31761	potassium channel
34	159.5	19.5	490	2	T26983	hypothetical prote
35	154.5	18.9	476	2	S21144	potassium channel
36	154.5	18.9	499	2	JH0313	potassium channel
37	154.5	18.9	499	2	I84204	potassium channel
38	154.5	18.9	499	2	A33814	potassium channel
39	153.5	18.8	499	2	I77466	potassium channel
40	153.5	18.8	499	2	A48672	delayed rectifier
41	151.5	18.6	256	2	C97062	potassium channel
42	151.5	18.6	484	2	T24238	hypothetical prote
43	149	18.3	528	2	T34417	delayed rectifier
44	147.5	18.1	428	2	A82873	potassium channel
45	146	17.9	494	2	JC5919	potassium channel

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### OM protein - protein search, using sw model

Run on: October 6, 2006, 18:10:58 ; Search time 302 Seconds  
(without alignments)  
490.074 Million cell updates/sec

Title: US-10-613-744-16

Perfect score: 816

Sequence: 1 MPPMLSGLLARLVKLLLGRH . . . . . TRALHERFDRLERMLDDNRR 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2:\*

1: uniprot sprot:\*

2: uniprot trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8

Result No.	Score	Match Length	DB	ID	Description
1	800	98.0	160	1 KCSA_STRCO	P0a333 streptomyce
2	800	98.0	160	1 KCSA_STRLI	P0a334 streptomyce
3	246	30.1	288	2 Q9FBY6_STRCO	Q9fbby6 streptomyce
4	244	29.9	244	2 Q4NH76_9MICC	Q4nh76 arthrobacter
5	234	28.7	241	2 Q8G6H7_BIFLO	Q8g6h7 bifidobacter
6	232	28.4	275	2 Q82BA6_STRAW	Q82ba6 streptomyce
7	222	27.2	280	2 Q9KMX2_VIBCH	Q9kmx2 vibrio chol
8	217.5	26.7	242	2 Q3E0I9_CHLAU	Q3e0i9 chloroflexus
9	217.5	26.7	264	2 Q5Z1J8_NOFCFA	Q5z1j8 nocardia fa
10	201.5	24.7	367	2 Q37FV5_RHOPA	Q37fv5 rhodopseudo
11	198.5	24.3	348	2 Q979Z2_THEVO	Q979z2 thermoplasma
12	198	24.3	280	2 Q3QL07_9GAMM	Q3ql07 shewanella
13	197.5	24.2	271	2 Q44GT4_CHRSL	Q44gt4 chromohalob
14	195.5	24.0	240	2 Q7MUC4_PORGI	Q7muc4 porphyromon
15	195.5	24.0	250	2 Q7MNY7_VIBVY	Q7mny7 vibrio vuln
16	195	23.9	269	2 Q3NRJ4_SHEFR	Q3nrj4 shewanella
17	191.5	23.5	250	2 Q8DEH4_VIBVU	Q8deh4 vibrio vuln
18	190.5	23.3	369	2 Q89CE1_BRAJA	Q89cel bradyrhizob
19	190	23.3	355	2 Q98GN8_RHILO	Q98gn8 rhizobium l
20	189	23.2	264	2 Q33XI4_9GAMM	Q33xi4 shewanella

21	188.5	23.1	487	2	Q26094_POLPE	Q26094 polyorchis
22	187	22.9	271	2	Q6LUZ8_PHOPR	Q6luz8 photobacter
23	187	22.9	273	2	Q2X1A0_9GAMM	Q2x1a0 shewanella
24	186.5	22.9	347	2	Q2W1V9_MAGSA	Q2w1v9 magnetospir
25	186	22.8	273	2	Q2ZTW5_SHEPU	Q2ztw5 shewanella
26	185.5	22.7	274	2	Q2Z5F3_9GAMM	Q2z5f3 shewanella
27	185.5	22.7	274	2	Q35S96_9GAMM	Q35s96 shewanella
28	185.5	22.7	274	2	Q364P7_9GAMM	Q364p7 shewanella
29	185	22.7	274	2	Q3Q0I8_9GAMM	Q3q0i8 shewanella
30	185	22.7	528	1	KCNA3_MOUSE	P16390 mus musculu
31	184.5	22.6	272	2	Q87SK2_VIBPA	Q87sk2 vibrio para
32	184.5	22.6	488	2	Q4SUC4_TETNG	Q4suc4 tetraodon n
33	183	22.4	276	2	Q3NXM5_9GAMM	Q3nxm5 shewanella
34	182.5	22.4	274	2	Q8EAX3_SHEON	Q8eax3 shewanella
35	181	22.2	523	1	KCNA3_HUMAN	P22001 homo sapien
36	181	22.2	525	1	KCNA3_RAT	P15384 rattus norv
37	181	22.2	557	2	Q6P2D3_HUMAN	Q6p2d3 homo sapien
38	181	22.2	575	2	Q5VWN2_HUMAN	Q5vwn2 homo sapien
39	180.5	22.1	269	2	Q3X4J7_9ACTN	Q3x4j7 rubrobacter
40	180	22.1	261	2	Q3C8L9_9CLOT	Q3c8l9 alkaliphilu
41	180	22.1	393	2	Q5VYU0_HUMAN	Q5vyu0 homo sapien
42	180	22.1	393	2	Q5UAX0_COLLI	Q5uax0 columba liv
43	180	22.1	436	2	Q5VYU1_HUMAN	Q5vyu1 homo sapien
44	180	22.1	516	2	Q28656_RABIT	Q28656 oryctolagus
45	180	22.1	615	2	Q5VYU2_HUMAN	Q5vyu2 homo sapien

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2006, 21:45:43 ; Search time 846 Seconds  
 (without alignments)  
 9568.298 Million cell updates/sec

Title: US-10-613-744-17

Perfect score: 1161

Sequence: 1 gcatgctggctccttggga.....ccatcgatgaacacagcatgc 1161

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
 1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1161	100.0	1161	2	AZ20116	Aaz20116 DNA encod
2	1161	100.0	1161	12	ADI38339	Adi38339 S. livida
3	1161	100.0	1161	15	AEE68565	Aee68565 Streptomy
4	288	24.8	554	6	AAI69258	Aai69258 Chimeric
5	288	24.8	555	6	AAI69254	Aai69254 Chimeric
6	288	24.8	555	6	AAI69259	Aai69259 Chimeric
7	288	24.8	555	6	AAI69253	Aai69253 Chimeric

8	288	24.8	555	6	AAI69260	Aai69260 Chimeric
9	282	24.3	555	6	AAI69252	Aai69252 Chimeric
10	239	20.6	555	6	AAI69255	Aai69255 Chimeric
11	234	20.2	555	6	AAI69257	Aai69257 Chimeric
12	221	19.0	555	6	AAI69250	Aai69250 Chimeric
13	221	19.0	555	6	AAI69251	Aai69251 Chimeric
14	198	17.1	555	6	AAI69256	Aai69256 Chimeric
c 15	22	1.9	771	11	ABD11069	Abd11069 Pseudomon
c 16	22	1.9	843	11	ABD11108	Abd11108 Pseudomon
17	22	1.9	3654	11	ABD10929	Abd10929 Pseudomon
18	21	1.8	36	6	AAI69270	Aai69270 Chimeric
c 19	21	1.8	67	6	AAI69264	Aai69264 S. livida
20	20	1.7	263	10	ADB90865	Adb90865 Human hyd
21	20	1.7	263	10	ADH61186	Adh61186 Human hyd
22	20	1.7	451	10	ADB90866	Adb90866 Human hyd
23	20	1.7	451	10	ADH61187	Adh61187 Human hyd
c 24	20	1.7	712	11	ACL31126	Ac131126 Rice abio
25	20	1.7	750	3	AAC77592	Aac77592 Human ORF
c 26	20	1.7	892	13	ADX64682	Adx64682 Plant ful
27	20	1.7	1050	11	ACL30546	Ac130546 Rice abio
c 28	20	1.7	1052	13	ADX59746	Adx59746 Plant ful
29	20	1.7	1053	11	ACL27524	Ac127524 Rice abio
c 30	20	1.7	1080	6	ABA99454	Aba99454 Actinopla
31	20	1.7	1173	8	ACA23753	Aca23753 Prokaryot
c 32	20	1.7	1179	12	ADI43256	Adi43256 Plant tra
c 33	20	1.7	1179	12	ADO02950	Ado02950 Corn orth
c 34	20	1.7	1299	15	AEF11677	Aef11677 Maize met
c 35	20	1.7	1305	12	ADI43257	Adi43257 Plant tra
c 36	20	1.7	1305	12	ADO02951	Ado02951 Corn orth
37	20	1.7	1613	15	AEE72138	Aee72138 Human tar
38	20	1.7	1621	4	AAC60228	Aac60228 Human hyd
39	20	1.7	1621	10	ADB90835	Adb90835 Human CDN
40	20	1.7	1621	10	ADH61156	Adh61156 Human hyd
c 41	20	1.7	1636	4	AAI60336	Aai60336 Human pol
42	20	1.7	1650	4	AAI58550	Aai58550 Human pol
43	20	1.7	1650	5	ADQ98767	Adq98767 DNA encod
44	20	1.7	1650	9	ADB48527	Adb48527 Novel hum
45	20	1.7	2400	8	ADA70795	Ada70795 Rice gene

## ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2006, 22:55:59 ; Search time 302 Seconds  
 (without alignments)  
 7146.862 Million cell updates/sec

Title: US-10-613-744-17

Perfect score: 1161

Sequence: 1 gcatgctggctccttggga.....ccatcgatgaacacgc 1161

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2386913 seqs, 929522941 residues

Word size : 1

Total number of hits satisfying chosen parameters: 4773488

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA\_New:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq:/\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:/\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:/\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:/\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:/\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:/\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:/\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1:/\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:/\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	23	2.0	1878	6	US-10-953-349-35151	Sequence 35151, A
2	23	2.0	1878	9	US-11-056-355B-8814	Sequence 8814, Ap
c 3	23	2.0	1976	9	US-11-218-305-12145	Sequence 12145, A
c 4	23	2.0	2494	9	US-11-218-305-12143	Sequence 12143, A
5	21	1.8	3250	9	US-11-218-305-18226	Sequence 18226, A
c 6	20	1.7	898	6	US-10-449-902-23732	Sequence 23732, A
7	20	1.7	1044	8	US-11-266-748A-98718	Sequence 98718, A
c 8	20	1.7	1044	8	US-11-266-748A-151529	Sequence 151529,
9	20	1.7	1089	8	US-11-266-748A-355547	Sequence 355547,
10	20	1.7	1089	8	US-11-266-748A-385372	Sequence 385372,
c 11	20	1.7	1089	8	US-11-266-748A-438926	Sequence 438926,
c 12	20	1.7	1179	6	US-10-374-780A-1719	Sequence 1719, Ap

c	13	20	1.7	1305	6	US-10-374-780A-1720	Sequence 1720, Ap
	14	20	1.7	1468	6	US-10-449-902-12256	Sequence 12256, A
	15	20	1.7	2173	9	US-11-218-305-8202	Sequence 8202, Ap
c	16	20	1.7	2356	9	US-11-218-305-9695	Sequence 9695, Ap
	17	20	1.7	3245	6	US-10-449-902-16228	Sequence 16228, A
c	18	19	1.6	150	8	US-11-217-529-3734	Sequence 3734, Ap
c	19	19	1.6	363	8	US-11-217-529-3731	Sequence 3731, Ap
	20	19	1.6	841	9	US-11-218-305-10221	Sequence 10221, A
c	21	19	1.6	980	9	US-11-174-307B-3361	Sequence 3361, Ap
c	22	19	1.6	1090	9	US-11-218-305-3109	Sequence 3109, Ap
c	23	19	1.6	1283	9	US-11-218-305-11135	Sequence 11135, A
c	24	19	1.6	1374	9	US-11-218-305-11134	Sequence 11134, A
	25	19	1.6	2247	9	US-11-218-305-10372	Sequence 10372, A
c	26	19	1.6	2356	6	US-10-449-902-25661	Sequence 25661, A
c	27	19	1.6	176594	6	US-10-539-228-495	Sequence 495, App
	28	18	1.6	490	8	US-11-266-748A-73470	Sequence 73470, A
	29	18	1.6	490	8	US-11-266-748A-107848	Sequence 107848,
c	30	18	1.6	490	8	US-11-266-748A-126281	Sequence 126281,
c	31	18	1.6	540	7	US-11-343-797-29	Sequence 29, Appl
	32	18	1.6	641	6	US-10-374-780A-1513	Sequence 1513, Ap
c	33	18	1.6	723	6	US-10-449-902-5315	Sequence 5315, Ap
	34	18	1.6	728	8	US-11-266-748A-10746	Sequence 10746, A
c	35	18	1.6	728	8	US-11-266-748A-64249	Sequence 64249, A
	36	18	1.6	728	8	US-11-266-748A-67081	Sequence 67081, A
	37	18	1.6	749	6	US-10-449-902-5217	Sequence 5217, Ap
c	38	18	1.6	772	6	US-10-449-902-20935	Sequence 20935, A
c	39	18	1.6	777	6	US-10-449-902-13675	Sequence 13675, A
	40	18	1.6	975	6	US-10-449-902-25906	Sequence 25906, A
	41	18	1.6	994	6	US-10-953-349-29239	Sequence 29239, A
	42	18	1.6	994	9	US-11-056-355B-64213	Sequence 64213, A
	43	18	1.6	1000	8	US-11-266-748A-395658	Sequence 395658,
c	44	18	1.6	1000	8	US-11-266-748A-466704	Sequence 466704,
	45	18	1.6	1043	8	US-11-266-748A-360224	Sequence 360224,

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2006, 19:43:42 ; Search time 7100 Seconds  
 (without alignments)  
 10456.754 Million cell updates/sec

Title: US-10-613-744-17

Perfect score: 1161

Sequence: 1 gcatgctggctccttggga.....ccatcgatgaacacagcatgc 1161

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : GenEmbl:  
 1: gb\_env:  
 2: gb\_pat:  
 3: gb\_ph:  
 4: gb\_pl:  
 5: gb\_pr:  
 6: gb\_ro:  
 7: gb\_sts:  
 8: gb\_sy:  
 9: gb\_un:  
 10: gb\_vl:  
 11: gb\_ov:  
 12: gb\_htg:  
 13: gb\_in:  
 14: gb\_om:  
 15: gb\_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
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1	1161	100.0	1161	2	AR428233	AR428233 Sequence
2	1151.4	99.2	1161	15	SLSKC1G	Z37969 S.lividans
3	1090.8	94.0	302007	15	SCO939132	AL939132 Streptomy
4	136.2	11.7	110000	15	CP000251_45	Continuation (46 o
c 5	123.2	10.6	110000	15	CP000251_11	Continuation (12 o
6	110	9.5	110000	15	BA000012_20	Continuation (21 o
7	109.4	9.4	294800	15	SME591789	AL591789 Sinorhizo

c	8	108.8	9.4	110000	15	AE014295_16	Continuation (17 o
c	9	108.8	9.4	349980	2	AX492783	AX492783 Sequence
c	10	108.8	9.4	349980	2	AX553950	AX553950 Sequence
c	11	97.8	8.4	110000	15	BA000030_24	Continuation (25 o
	12	92	7.9	110000	15	BA000040_86	Continuation (87 o
c	13	90.2	7.8	110000	15	BA000030_69	Continuation (70 o
c	14	90.2	7.8	110000	15	BA000030_70	Continuation (71 o
c	15	89.8	7.7	110000	15	AP006618_09	Continuation (10 o
	16	88	7.6	110000	15	CP000133_29	Continuation (30 o
c	17	85.8	7.4	303450	15	SCO939130	AL939130 Streptomy
c	18	83.4	7.2	125020	5	AF429315	AF429315 Homo sapi
c	19	83.2	7.2	159997	12	CR352334	CR352334 Danio rer
c	20	81.2	7.0	110000	15	BA000030_33	Continuation (34 o
	21	80.2	6.9	110000	15	AE017180_05	Continuation (6 of
	22	77.6	6.7	125020	5	AF429315	AF429315 Homo sapi
c	23	75.4	6.5	110000	15	CP000251_13	Continuation (14 o
	24	75	6.5	2019	8	AY320286	AY320286 Synthetic
c	25	73.6	6.3	110000	15	CP000251_10	Continuation (11 o
	26	72.8	6.3	110000	15	CP000251_16	Continuation (17 o
c	27	72.6	6.3	110000	15	AP007255_36	Continuation (37 o
	28	71.8	6.2	2859	2	AX798520	AX798520 Sequence
	29	71.8	6.2	6040	2	AX798519	AX798519 Sequence
c	30	71.6	6.2	110000	15	CP000251_44	Continuation (45 o
	31	70.8	6.1	110000	15	CP000251_37	Continuation (38 o
	32	70.6	6.1	896	2	BD074155	BD074155 KCNQ pota
	33	70.6	6.1	896	2	AR213244	AR213244 Sequence
c	34	70.6	6.1	295150	15	SCO939125	AL939125 Streptomy
	35	70.4	6.1	1780	14	CFU08596	U08596 Canis famil
	36	70.4	6.1	1803	14	AY204505	AY204505 Canis fam
	37	70.4	6.1	1872	14	AF056943	AF056943 Oryctolag
	38	69.8	6.0	110000	15	CP000133_33	Continuation (34 o
	39	68.8	5.9	1814	14	AF149787	AF149787 Oryctolag
c	40	68.6	5.9	11095	15	AE004359	AE004359 Vibrio ch
c	41	68.6	5.9	110000	15	BA000002_06	Continuation (7 of
c	42	68.4	5.9	110000	15	BA000040_63	Continuation (64 o
	43	68.2	5.9	1803	14	AY635585	AY635585 Sus scrof
	44	68	5.9	2765	13	AB212761	AB212761 Nephila c
c	45	67.8	5.8	110000	15	CP000251_17	Continuation (18 o

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2006, 19:42:02 ; Search time 849 Seconds  
 (without alignments)  
 9534.488 Million cell updates/sec

Title: US-10-613-744-17

Perfect score: 1161

Sequence: 1 gcatgctggctccttggga.....ccatcgatgaacagcatgc 1161

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : N\_Geneseq\_8:  
 1: geneseqn1980s:  
 2: geneseqn1990s:  
 3: geneseqn2000s:  
 4: geneseqn2001as:  
 5: geneseqn2001bs:  
 6: geneseqn2002as:  
 7: geneseqn2002bs:  
 8: geneseqn2003as:  
 9: geneseqn2003bs:  
 10: geneseqn2003cs:  
 11: geneseqn2003ds:  
 12: geneseqn2004as:  
 13: geneseqn2004bs:  
 14: geneseqn2005s:  
 15: geneseqn2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1161	100.0	1161	2	AAZ20116	Aaz20116 DNA encod
2	1161	100.0	1161	12	ADI38339	Adi38339 S. livida
3	1161	100.0	1161	15	AEE68565	Aee68565 Streptomy
4	465	40.1	555	6	AAI69254	Aai69254 Chimeric
5	460.2	39.6	555	6	AAI69257	Aai69257 Chimeric
6	445.8	38.4	555	6	AAI69259	Aai69259 Chimeric
7	445.8	38.4	555	6	AAI69253	Aai69253 Chimeric

8	444.2	38.3	554	6	AAI69258	Aai69258 Chimeric
9	444.2	38.3	555	6	AAI69255	Aai69255 Chimeric
10	444.2	38.3	555	6	AAI69260	Aai69260 Chimeric
11	442.6	38.1	555	6	AAI69252	Aai69252 Chimeric
12	429.8	37.0	555	6	AAI69256	Aai69256 Chimeric
13	417	35.9	555	6	AAI69251	Aai69251 Chimeric
14	412.2	35.5	555	6	AAI69250	Aai69250 Chimeric
c	15	108.8	9.4	349980	6	ABQ81845
	16	71.8	6.2	2859	10	ADF30786
	17	71.8	6.2	6040	10	ADF30785
	18	70.8	6.1	114955	2	AAX53491
	19	68.6	5.9	843	8	ACA53539
	20	66.4	5.7	4234	10	ADC77662
	21	66.4	5.7	4234	13	ADQ89061
	22	66.4	5.7	4234	13	ADR44891
	23	66.4	5.7	4237	14	ADX05898
	24	66.4	5.7	5999	8	ABX34702
	25	66.4	5.7	6001	8	ABX34526
	26	65.6	5.7	1836	5	AAH21452
	27	65.6	5.7	2118	10	ACA56706
	28	65.6	5.7	2118	12	ADI56502
	29	65.6	5.7	2865	14	ADX18984
c	30	65.6	5.7	2867	6	ABL65917
	31	65.6	5.7	2867	6	ABN95856
	32	65.4	5.6	114955	2	AAX53491
	33	63.4	5.5	9222	8	AAL61171
	c	34	63.4	5.5	82746	Aal61224 Actinosyn
	35	63	5.4	15738	10	ADI23898
	36	63	5.4	37360	10	ADI23892
	37	62.2	5.4	1182	2	AAT85964
	38	62.2	5.4	1425	6	ABK64418
	39	62.2	5.4	1425	10	ADD49930
	40	62.2	5.4	1848	12	ADH51119
	41	62.2	5.4	1848	12	ADM77995
	42	62.2	5.4	1848	14	AEA48082
	43	62.2	5.4	1878	12	ADH51117
	44	62.2	5.4	1878	12	ADM77993
	45	62.2	5.4	1878	14	Aea48080 cDNA enco
						Adm77993 KCNQ2-15b
						Adh51117 Potassium
						Adm77995 KCNQ2-15b
						Aea48082 cDNA enco
						Adh51117 Potassium
						Adm77993 KCNQ2-15b
						Aea48080 cDNA enco

## ALIGNMENTS

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2006, 19:53:57 ; Search time 262 Seconds  
 (without alignments)  
 8291.440 Million cell updates/sec

Title: US-10-613-744-17

Perfect score: 1161

Sequence: 1 gcatgctggctccttggga.....ccatcgatgaacacgc 1161

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

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3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PECTUS\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1161	100.0	1161	3	US-09-275-252A-17	Sequence 17, Appl
2	70.6	6.1	896	3	US-09-105-058C-1	Sequence 1, Appli
3	66.4	5.7	4234	3	US-09-949-016-325	Sequence 325, App
4	66.4	5.7	4237	3	US-09-949-016-2146	Sequence 2146, Ap
5	66.4	5.7	8237	3	US-09-949-016-12067	Sequence 12067, A
6	66.4	5.7	8237	3	US-09-949-016-13888	Sequence 13888, A
7	65.6	5.7	2118	3	US-09-016-434-1304	Sequence 1304, AP
8	65.6	5.7	2867	4	US-09-880-107-2354	Sequence 2354, Ap
9	62.2	5.4	900	3	US-09-105-058C-3	Sequence 3, Appli
10	62.2	5.4	3232	3	US-09-177-650-1	Sequence 1, Appli

11	62.2	5.4	3237	3	US-09-177-650-95	Sequence 95, Appl
12	62.2	5.4	3287	3	US-09-105-058C-19	Sequence 19, Appl
13	62	5.3	1288	2	US-08-440-856A-9	Sequence 9, Appli
c 14	61.4	5.3	40138	3	US-09-090-793-12	Sequence 12, Appl
c 15	61.4	5.3	40138	3	US-09-231-899-12	Sequence 12, Appl
16	60	5.2	2196	3	US-09-949-016-1823	Sequence 1823, Ap
17	59.6	5.1	3004	3	US-09-949-016-324	Sequence 324, App
18	59.6	5.1	3004	3	US-09-949-016-2293	Sequence 2293, Ap
19	59.6	5.1	7055	3	US-09-949-016-12066	Sequence 12066, A
20	59.6	5.1	7056	3	US-09-949-016-14035	Sequence 14035, A
c 21	58.8	5.1	513	3	US-09-252-991A-2092	Sequence 2092, Ap
22	58.8	5.1	1500	3	US-09-252-991A-1868	Sequence 1868, Ap
23	58.8	5.1	1737	3	US-09-252-991A-1717	Sequence 1717, Ap
c 24	58.8	5.1	1767	3	US-09-252-991A-2007	Sequence 2007, Ap
25	58.6	5.0	1455	5	US-10-114-270-43	Sequence 43, Appl
26	58.6	5.0	1638	3	US-09-833-466-2	Sequence 2, Appli
27	58.6	5.0	2103	3	US-09-833-466-1	Sequence 1, Appli
28	58.4	5.0	2335	3	US-09-492-361-1	Sequence 1, Appli
29	57.6	5.0	1746	3	US-09-758-759-92	Sequence 92, Appl
30	57.6	5.0	109519	3	US-09-758-759-1	Sequence 1, Appli
31	57.2	4.9	1728	3	US-09-758-759-126	Sequence 126, App
32	57.2	4.9	5760	3	US-10-152-886-14	Sequence 14, Appl
33	56.4	4.9	1802	3	US-09-949-016-1604	Sequence 1604, Ap
34	56.4	4.9	5802	3	US-09-949-016-13346	Sequence 13346, A
35	56	4.8	601	3	US-09-949-016-55210	Sequence 55210, A
36	55.8	4.8	735	3	US-09-105-058C-7	Sequence 7, Appli
37	55.8	4.8	5811	3	US-10-152-886-2	Sequence 2, Appli
38	54.6	4.7	888	3	US-09-252-991A-11022	Sequence 11022, A
39	54.6	4.7	1197	3	US-09-252-991A-10946	Sequence 10946, A
40	54.4	4.7	2273	3	US-09-177-650-88	Sequence 88, Appl
41	53.4	4.6	1707	3	US-09-724-797-15	Sequence 15, Appl
42	53.4	4.6	2007	3	US-09-902-540-9461	Sequence 9461, Ap
c 43	53.4	4.6	15095	3	US-09-902-540-1077	Sequence 1077, Ap
44	53.2	4.6	2483	2	US-08-464-340A-3	Sequence 3, Appli
45	53.2	4.6	2483	7	PCT-US94-08449A-3	Sequence 3, Appli

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2006, 19:58:01 ; Search time 1742 Seconds  
 (without alignments)  
 8189.406 Million cell updates/sec

Title: US-10-613-744-17

Perfect score: 1161

Sequence: 1 gcatgctggctccttggga.....ccatcgatgaacagcatgc 1161

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*

11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*

12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*

13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*

14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*

15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*

16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
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1	1161	100.0	1161	10	US-10-613-744-17	Sequence 17, Appl
c 2	108.8	9.4	2256646	8	US-10-470-565-1	Sequence 1, Appli
c 3	97.8	8.4	9025608	7	US-10-156-761-1	Sequence 1, Appli
4	96.8	8.3	606	7	US-10-156-761-1981	Sequence 1981, Ap
5	90.2	7.8	825	7	US-10-156-761-5778	Sequence 5778, Ap
6	81.2	7.0	3471	7	US-10-156-761-2726	Sequence 2726, Ap

7	71.8	6.2	2859	9	US-10-872-874-6	Sequence 6, Appli
8	71.8	6.2	6040	9	US-10-872-874-5	Sequence 5, Appli
9	70.6	6.1	896	6	US-10-128-870-1	Sequence 1, Appli
10	70.6	6.1	896	6	US-10-131-685-1	Sequence 1, Appli
11	68.6	5.9	843	8	US-10-282-122A-41409	Sequence 41409, A
12	66.4	5.7	4234	7	US-10-369-022-25	Sequence 25, Appli
13	66.4	5.7	4234	9	US-10-757-262-13	Sequence 13, Appli
14	66.4	5.7	4234	9	US-10-768-158-9	Sequence 9, Appli
15	65.8	5.7	748	9	US-10-425-115-103143	Sequence 103143,
16	65.6	5.7	1400	13	US-11-060-756-3854	Sequence 3854, Ap
17	65.6	5.7	1400	13	US-11-060-756-3855	Sequence 3855, Ap
18	65.6	5.7	1400	13	US-11-060-756-8126	Sequence 8126, Ap
19	65.6	5.7	1400	13	US-11-060-756-8127	Sequence 8127, Ap
20	65.6	5.7	1836	3	US-09-758-036-5	Sequence 5, Appli
21	65.6	5.7	2118	7	US-10-305-720-1304	Sequence 1304, Ap
22	65.6	5.7	2867	3	US-09-954-456-1227	Sequence 1227, Ap
23	65.6	5.7	2867	3	US-09-880-107-2354	Sequence 2354, Ap
24	65.6	5.7	2867	10	US-10-843-641A-4254	Sequence 4254, Ap
25	63.4	5.5	9222	12	US-10-496-351-2	Sequence 2, Appli
c 26	63.4	5.5	82746	12	US-10-496-351-56	Sequence 56, Appli
27	63	5.4	15738	7	US-10-329-079-12	Sequence 12, Appli
28	63	5.4	37360	7	US-10-329-079-6	Sequence 6, Appli
29	62.2	5.4	900	6	US-10-128-870-3	Sequence 3, Appli
30	62.2	5.4	900	6	US-10-131-685-3	Sequence 3, Appli
31	62.2	5.4	1425	3	US-09-960-706-511	Sequence 511, App
32	62.2	5.4	1425	3	US-09-873-319-313	Sequence 313, App
33	62.2	5.4	1425	7	US-10-116-712-662	Sequence 662, App
34	62.2	5.4	1848	9	US-10-744-796-5	Sequence 5, Appli
35	62.2	5.4	1878	9	US-10-744-796-3	Sequence 3, Appli
36	62.2	5.4	1932	9	US-10-744-796-1	Sequence 1, Appli
37	62.2	5.4	2619	7	US-10-345-680-18	Sequence 18, Appli
38	62.2	5.4	2750	10	US-10-399-489A-2	Sequence 2, Appli
39	62.2	5.4	3195	10	US-10-450-763-10635	Sequence 10635, A
40	62.2	5.4	3232	7	US-10-345-680-16	Sequence 16, Appli
41	62.2	5.4	3232	7	US-10-096-578-1	Sequence 1, Appli
42	62.2	5.4	3232	8	US-10-820-307-1	Sequence 1, Appli
43	62.2	5.4	3232	10	US-10-450-763-10634	Sequence 10634, A
44	62.2	5.4	3237	7	US-10-096-578-95	Sequence 95, Appli
45	62.2	5.4	3287	6	US-10-128-870-19	Sequence 19, Appli

## ALIGNMENTS

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2006, 21:41:22 ; Search time 303 Seconds  
 (without alignments)  
 7123.275 Million cell updates/sec

Title: US-10-613-744-17

Perfect score: 1161

Sequence: 1 gcatgctggctccttggga.....ccatcgatgaacacatgc 1161

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 2386913 seqs, 929522941 residues

Total number of hits satisfying chosen parameters: 4773826

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_NA\_New:  
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 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1:\*
 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*
 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	66.4	5.7	4234	8 US-11-312-958-25	Sequence 25, Appl
2	65.6	5.7	1917	7 US-11-317-847A-97	Sequence 97, Appl
3	65.6	5.7	2865	6 US-10-565-185-17	Sequence 17, Appl
4	65.6	5.7	2865	8 US-11-266-748A-29247	Sequence 29247, A
5	65	5.6	777	8 US-11-266-748A-433	Sequence 433, App
6	62.2	5.4	1425	7 US-11-363-917-4	Sequence 4, Appl
7	62.2	5.4	1848	6 US-10-519-335-5	Sequence 5, Appl
8	62.2	5.4	1878	6 US-10-519-335-3	Sequence 3, Appl
9	62.2	5.4	1932	6 US-10-519-335-1	Sequence 1, Appl
10	62.2	5.4	2565	7 US-11-363-917-2	Sequence 2, Appl
11	62.2	5.4	2619	8 US-11-302-678-18	Sequence 18, Appl
12	62.2	5.4	3232	8 US-11-302-678-16	Sequence 16, Appl

13	60	5.2	1791	7	US-11-330-123-83	Sequence 83, Appl	
14	60	5.2	9762	7	US-11-330-123-73	Sequence 73, Appl	
15	59.6	5.1	3004	6	US-10-539-228-95	Sequence 95, Appl	
16	59.6	5.1	3025	6	US-10-669-920-920	Sequence 920, App	
17	59.6	5.1	3058	6	US-10-669-920-918	Sequence 918, App	
18	59.6	5.1	3058	6	US-10-669-920-922	Sequence 922, App	
19	59.6	5.1	23055	6	US-10-539-228-94	Sequence 94, Appl	
20	59.6	5.1	23237	6	US-10-669-920-917	Sequence 917, App	
21	58.8	5.1	1468	6	US-10-449-902-12256	Sequence 12256, A	
22	58.6	5.0	2094	6	US-10-474-894-21	Sequence 21, Appl	
23	58.4	5.0	1771	9	US-11-174-307B-927	Sequence 927, App	
24	58.4	5.0	1771	9	US-11-056-355B-16510	Sequence 16510, A	
25	57.8	5.0	2048	6	US-10-449-902-13093	Sequence 13093, A	
26	57.6	5.0	1420	6	US-10-534-744-1	Sequence 1, Appli	
27	57.4	4.9	1260	7	US-11-317-847A-63	Sequence 63, Appl	
28	57.4	4.9	1260	7	US-11-317-847A-67	Sequence 67, Appl	
29	57.4	4.9	1260	7	US-11-317-847A-69	Sequence 69, Appl	
30	57.4	4.9	1260	7	US-11-317-847A-71	Sequence 71, Appl	
31	57.4	4.9	1260	7	US-11-317-847A-73	Sequence 73, Appl	
32	57.4	4.9	1260	7	US-11-317-847A-75	Sequence 75, Appl	
33	57.4	4.9	1260	7	US-11-317-847A-77	Sequence 77, Appl	
34	57.4	4.9	1260	7	US-11-317-847A-79	Sequence 79, Appl	
35	57.4	4.9	1278	7	US-11-317-847A-59	Sequence 59, Appl	
36	57.4	4.9	1278	7	US-11-317-847A-61	Sequence 61, Appl	
37	57.4	4.9	1278	7	US-11-317-847A-65	Sequence 65, Appl	
c	38	57.4	4.9	1513	9	US-11-218-305-18568	Sequence 18568, A
	39	57	4.9	1957	6	US-10-953-349-33932	Sequence 33932, A
	40	57	4.9	1957	9	US-11-174-307B-2191	Sequence 2191, Ap
	41	57	4.9	1957	9	US-11-056-355B-10679	Sequence 10679, A
	42	57	4.9	1981	9	US-11-218-305-6625	Sequence 6625, Ap
	43	57	4.9	7459	9	US-11-218-305-6624	Sequence 6624, Ap
	44	56.8	4.9	36602	7	US-11-330-123-1	Sequence 1, Appli
	45	56.4	4.9	1000	8	US-11-266-748A-395658	Sequence 395658,

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2006, 19:51:37 ; Search time 6430 Seconds  
 (without alignments)  
 10096.788 Million cell updates/sec

Title: US-10-613-744-17

Perfect score: 1161

Sequence: 1 gcatgctggctccttggga.....ccatcgatgaacacagcatgc 1161

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

 1: gb\_est1:\*
   
 2: gb\_est3:\*
   
 3: gb\_est4:\*
   
 4: gb\_est5:\*
   
 5: gb\_est6:\*
   
 6: gb\_htc:\*
   
 7: gb\_est2:\*
   
 8: gb\_est7:\*
   
 9: gb\_est8:\*
   
 10: gb\_est9:\*
   
 11: gb\_gss1:\*
   
 12: gb\_gss2:\*
   
 13: gb\_gss3:\*
   
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
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c 1	82.2	7.1	1394	9	DN696455	DN696455 CLJ07-A09
c 2	80.4	6.9	1542	14	AG032943	AG032943 Pan trogl
c 3	76.4	6.6	1332	1	AM105094	AM105094 AM105094
c 4	76	6.5	671	9	DN265257	DN265257 LIB30320_
5	75	6.5	1428	10	DV779809	DV779809 Hw_Fat_35
6	73.2	6.3	925	14	CNS0091P	AL053013 Drosophil
c 7	72.8	6.3	935	14	CNS006XK	AL066051 Drosophil
c 8	70.4	6.1	1260	10	DT966447	DT966447 CLJ104-H0

9	70.4	6.1	1569	14	AG341503	AG341503 Mus muscu
10	70.4	6.1	2017	14	AG435283	AG435283 Mus muscu
11	70	6.0	1094	14	AG036373	AG036373 Pan trogl
12	70	6.0	1209	9	DN696456	DN696456 CLJ07-A09
c 13	69.8	6.0	1151	5	CK210749	CK210749 FGAS02257
14	69.6	6.0	1359	13	CL507830	CL507830 SAIL_788_
15	69.4	6.0	1798	14	AG171124	AG171124 Pan trogl
c 16	68.6	5.9	1165	14	AG030649	AG030649 Pan trogl
17	68.2	5.9	855	3	BU963646	BU963646 AGENCOURT
18	68	5.9	1018	10	DV012412	DV012412 CNB274-E0
c 19	68	5.9	1798	14	AG171124	AG171124 Pan trogl
c 20	68	5.9	2332	14	AG363333	AG363333 Mus muscu
21	67.6	5.8	1151	5	CK210749	CK210749 FGAS02257
22	67.2	5.8	1116	2	BG810038	BG810038 mgct002xi
23	67.2	5.8	1838	14	DQ052673	DQ052673 Pan trogl
24	67	5.8	1100	14	CNS016KD	AL106855 Drosophil
c 25	67	5.8	1250	14	AG043469	AG043469 Pan trogl
c 26	66.8	5.8	932	14	CNS0072Q	AL066742 Drosophil
c 27	66.6	5.7	900	14	CNS02RD3	AL210432 Tetraodon
28	66.6	5.7	986	14	AG074680	AG074680 Pan trogl
c 29	66.6	5.7	1085	10	DW609933	DW609933 CLJ253-H0
30	66.6	5.7	1821	12	CL090560	CL090560 ISB1-17N1
c 31	66.4	5.7	925	14	CNS0091P	AL053013 Drosophil
32	66.4	5.7	1374	14	AY412410	AY412410 Homo sapi
33	66	5.7	1299	14	AG039481	AG039481 Pan trogl
34	65.8	5.7	874	12	CG317023	CG317023 OGWB154TH
c 35	65.8	5.7	879	12	CG286328	CG286328 OGXR01TV
36	65.8	5.7	941	12	CC733589	CC733589 OGVBK91TV
37	65.8	5.7	1355	3	BM906309	BM906309 AGENCOURT
c 38	65.8	5.7	1474	13	CL500927	CL500927 SAIL_68_H
39	65.6	5.7	1842	14	DQ052672	DQ052672 Homo sapi
c 40	65.2	5.6	1164	14	AG128373	AG128373 Pan trogl
41	64.8	5.6	542	4	BX280957	BX280957 BX280957
c 42	64.8	5.6	1284	2	BM547577	BM547577 AGENCOURT
43	64.4	5.5	1409	2	BG850730	BG850730 1024029B1
44	64.2	5.5	1278	14	AG060116	AG060116 Pan trogl
c 45	64.2	5.5	1956	12	CG754548	CG754548 P050-1-A1